```
GAGCTCGGAT CCACTACTCG ACCCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG      60

CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA     120

TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA      175
                                         Met Arg Arg Ala Ser Arg
                                          1               5

GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC       223
Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
            10                  15                  20

GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT       271
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
        25                  30                  35

CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG       319
Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
    40                  45                  50
```

FIG.1A

```
GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC      367
Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
 55                  60                  65                  70

TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC      415
Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
                 75                  80                  85

TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC      463
Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp
             90                  95                 100

TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG      511
Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
        105                 110                 115

AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG      559
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
    120                 125                 130
```

FIG.1B

```
GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG      607
Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
135                 140                 145                 150

TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC      655
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
                155                 160                 165

CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT      703
Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
            170                 175                 180

CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG      751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met
        185                 190                 195
```

FIG.1C

```
ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC      799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
    200                 205                 210

CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA      847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
215                 220                 225                 230

CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC      895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile
                235                 240                 245

AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC      943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
            250                 255                 260

TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA      991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
        265                 270                 275
```

FIG.1D

```
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC      1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
    280                 285                 290

CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC      1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
295                 300                 305                 310

AAA GTT CAG GAC ATA GAC T GAGACTCATT TCGTGGAACA TTAGCATGGA           1136
Lys Val Gln Asp Ile Asp
                315

TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA    1196

CTAAGAGACA TGGCCCACGG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG    1256

TTGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTCATG GTGATTACAC AACGGTTTTA    1316
```

FIG.1E

CAATTTTGTA ATGATTTCCT AGAATTGAAC CAGATTGGGA GAGGTATTCC GATGCTTATG 1376

AAAAACTTAC ACGTGAGCTA TGGAAGGGGG TCACAGTCTC TGGGTCTAAC CCCTGGACAT 1436

GTGCCACTGA GAACCTTGAA ATTAAGAGGA TGCCATGTCA TTGCAAAGAA ATGATAGTGT 1496

GAAGGGTTAA GTTCTTTTGA ATTGTTACAT TGCGCTGGGA CCTGCAAATA AGTTCTTTTT 1556

TTCTAATGAG GAGAGAAAAA TATATGTATT TTTATATAAT GTCTAAAGTT ATATTTCAGG 1616

TGTAATGTTT TCTGTGCAAA GTTTTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA 1676

ATATTTAAAA ATGTCTCACT GTTGACATAT TTAATGTTTT AAATGTACAG ATGTATTTAA 1736

CTGGTGCACT TTGTAATTCC CCTGAAGGTA CTCGTAGCTA AGGGGGCAGA ATACTGTTTC 1796

TGGTGACCAC ATGTAGTTTA TTTCTTTATT CTTTTTAACT TAATAGAGTC TTCAGACTTG 1856

FIG.1F

```
TCAAAACTAT GCAAGCAAAA TAAATAAATA AAAATAAAAT GAATACCTTG AATAATAAGT    1916

AGGATGTTGG TCACCAGGTG CCTTTCAAAT TTAGAAGCTA ATTGACTTTA GGAGCTGACA    1976

TAGCCAAAAA GGATACATAA TAGGCTACTG AAATCTGTCA GGAGTATTTA TGCAATTATT    2036

GAACAGGTGT CTTTTTTTAC AAGAGCTACA AATTGTAAAT TTTGTTTCTT TTTTTTCCCA    2096

TAGAAAATGT ACTATAGTTT ATCAGCCAAA AAACAATCCA CTTTTTAATT TAGTGAAAGT    2156

TATTTTATTA TACTGTACAA TAAAAGCATT GTCTCTGAAT GTTAATTTTT TGGTACAAAA    2216

AATAAATTTG TACGAAAACC TGAAAAAAAA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCT    2276

AGAGGGCCCT ATTCTATAG                                                 2295
```

FIG.1G

FIG.2A

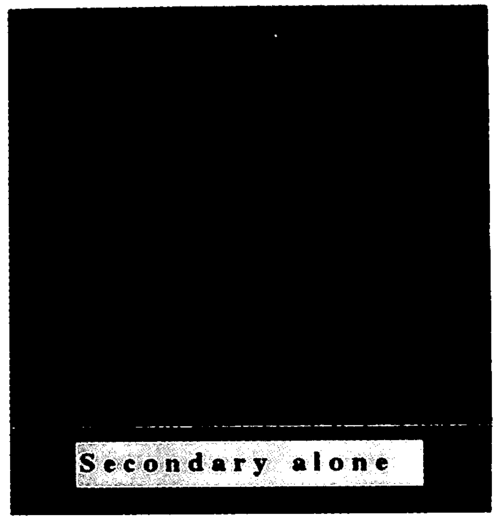


FIG.2B

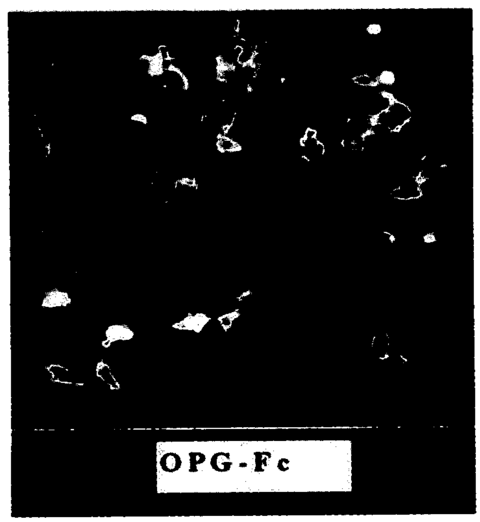
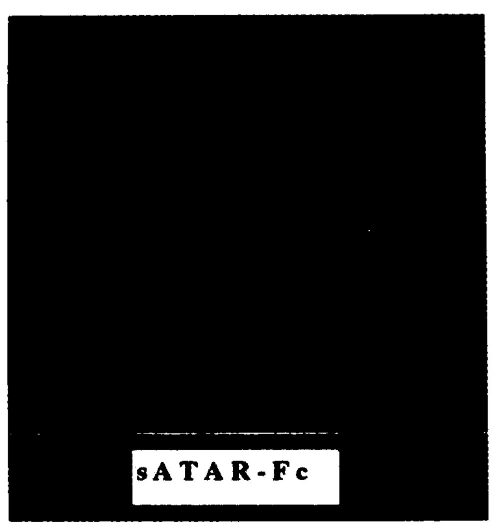


FIG.2C



Title: OSTEOPROTEGERIN BINDING PROTEINS AND RECEPTORS
Inventor: William J. Boyle
Docket No a-451N

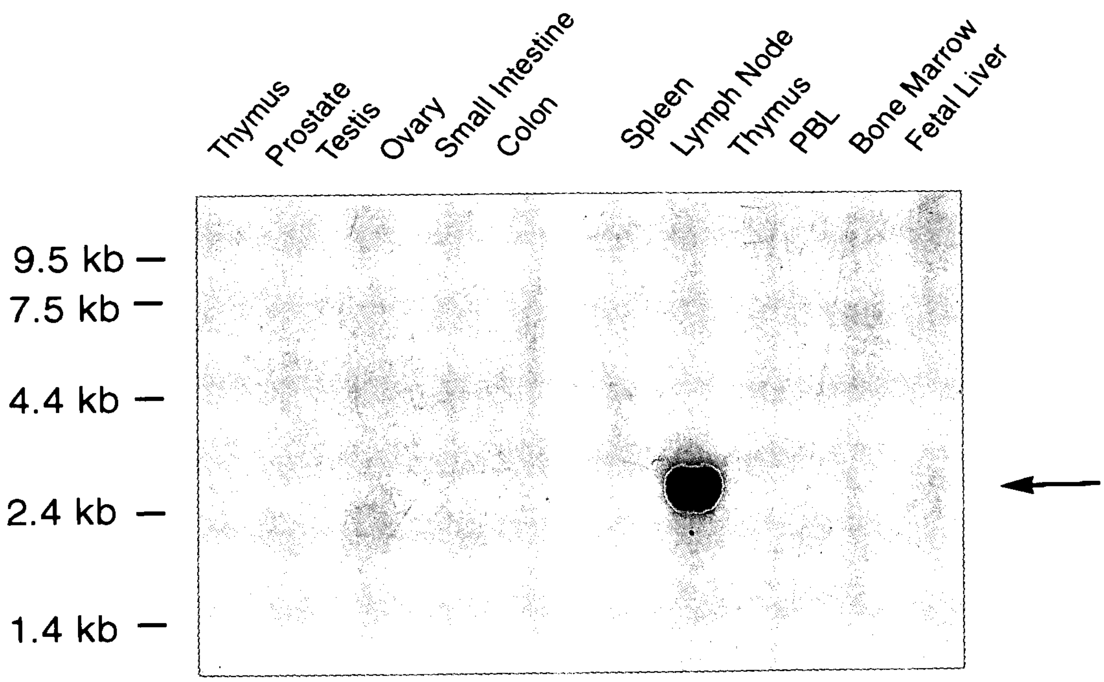


FIG.3

```
          10                  30                  50
AAGCTTGGTACCGAGCTCGGATCCACTACTCGACCCACGCGTCCGCGCCCCAGGAGCC

          70                  90                 110
AAAGCCGGGCTCCAAGTCGGCGCCCCACGTCGAGGCTCCGCCGCAGCCTCCGGAGTTGGC

         130                 150                 170
CGCAGACAAGAAGGGGAGGGAGCGGGAGAGGGAGGAGAGCTCCGAAGCGAGAGGGCCGAG

         190                 210                 230
CGCCATGCGCCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGG
    M  R  R  A  S  R  D  Y  T  K  Y  L  R  G  S  E  E  M  G

         250                 270                 290
CGGCGGCCCCGGAGCCCCGCACGAGGGCCCCCTGCACGCCCCGCCGCCGCCTGCGCCGCA
 G  G  P  G  A  P  H  E  G  P  L  H  A  P  P  P  P  A  P  H

         310                 330                 350
CCAGCCCCCCGCCGCCTCCCGCTCCATGTTCGTGGCCCTCCTGGGGCTGGGGCTGGGCCA
 Q  P  P  A  A  S  R  S  M  F  V  A  L  L  G  L  G  L  G  Q

         370                 390                 410
GGTTGTCTGCAGCGTCGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAAT
 V  V  C  S  V  A  L  F  F  Y  F  R  A  Q  M  D  P  N  R  I
```

FIG.4A

```
        430                 450                 470
ATCAGAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTT
 S  E  D  G  T  H  C  I  Y  R  I  L  R  L  H  E  N  A  D  F

        490                 510                 530
TCAAGACACAACTCTGGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGGAGAAT
 Q  D  T  T  L  E  S  Q  D  T  K  L  I  P  D  S  C  R  R  I

        550                 570                 590
TAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCA
 K  Q  A  F  Q  G  A  V  Q  K  E  L  Q  H  I  V  G  S  Q  H

        610                 630                 650
CATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAA
 I  R  A  E  K  A  M  V  D  G  S  W  L  D  L  A  K  R  S  K

        670                 690                 710
GCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTC
 L  E  A  Q  P  F  A  H  L  T  I  N  A  T  D  I  P  S  G  S

        730                 750                 770
CCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACAT
 H  K  V  S  L  S  S  W  Y  H  D  R  G  W  A  K  I  S  N  M
```

FIG.4B

```
          790                           810                           830
GACTTTTAGCAATGGAAAACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAA
 T  F  S  N  G  K  L  I  V  N  Q  D  G  F  Y  Y  L  Y  A  N

          850                           870                           890
CATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAAT
 I  C  F  R  H  H  E  T  S  G  D  L  A  T  E  Y  L  Q  L  M

          910                           930                           950
GGTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAGG
 V  Y  V  T  K  T  S  I  K  I  P  S  S  H  T  L  M  K  G  G

          970                           990                          1010
AAGCACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTTATTCCATAAACGTTGGTGG
 S  T  K  Y  W  S  G  N  S  E  F  H  F  Y  S  I  N  V  G  G

         1030                          1050                          1070
ATTTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACT
 F  F  K  L  R  S  G  E  E  I  S  I  E  V  S  N  P  S  L  L

         1090                          1110                          1130
GGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCGAGATATAGATTGAGC
 D  P  D  Q  D  A  T  Y  F  G  A  F  K  V  R  D  I  D
```

FIG.4C

```
       1150                1170                1190
CCCAGTTTTTGGAGTGTTATGTATTTCCTGGATGTTTGGAAACATTTTTTAAAACAAGCC

       1210                1230                1250
AAGAAAGATGTATATAGGTGTGTGAGACTACTAAGAGGCATGGCCCCAACGGTACACGAC

       1270                1290                1310
TCAGTATCCATGCTCTTGACCTTGTAGAGAACACGCGTATTTACAGCCAGTGGGAGATGT

       1330                1350                1370
TAGACTCATGGTGTGTTACACAATGGTTTTTAAATTTTGTAATGAATTCCTAGAATTAAA

       1390                1410                1430
CCAGATTGGAGCAATTACGGGTTGACCTTATGAGAAACTGCATGTGGGCTATGGGAGGGG
```

FIG.4D

```
       1450                1470                1490
TTGGTCCCTGGTCATGTGCCCCTTCGCAGCTGAAGTGGAGAGGGTGTCATCTAGCGCAAT

       1510                1530                1550
TGAAGGATCATCTGAAGGGGCAAATTCTTTTGAATTGTTACATCATGCTGGAACCTGCAA

       1570                1590                1610
AAAATACTTTTTCTAATGAGGAGAGAAAATATATGTATTTTTATATAATATCTAAAGTTA

       1630                1650                1670
TATTTCAGATGTAATGTTTTCTTTGCAAAGTATTGTAAATTATATTTGTGCTATAGTATT

       1690                1710                1730
TGATTCAAAATATTTAAAAATGTCTTGCTGTTGACATATTTAATGTTTTAAATGTACAGA

       1750                1770                1790
CATATTTAACTGGTGCACTTTGTAAATTCCCTGGGGAAAACTTGCAGCTAAGGAGGGGAA

       1810                1830                1850
AAAAATGTTGTTTCCTAATATCAAATGCAGTATATTTCTTCGTTCTTTTTAAGTTAATAG
```

FIG.4E

```
        1870                1890                1910
ATTTTTTCAGACTTGTCAAGCCTGTGCAAAAAAATTAAAATGGATGCCTTGAATAATAAG

        1930                1950                1970
CAGGATGTTGGCCACCAGGTGCCTTTCAAATTTAGAAACTAATTGACTTTAGAAAGCTGA

        1990                2010                2030
CATTGCCAAAAAGGATACATAATGGGCCACTGAAATCTGTCAAGAGTAGTTATATAATTG

        2050                2070                2090
TTGAACAGGTGTTTTTCCACAAGTGCCGCAAATTGTACCTTTTTTTTTTTTTCAAAATAG

        2110                2130                2150
AAAAGTTATTAGTGGTTTATCAGCAAAAAAGTCCAATTTTAATTTAGTAAATGTTATCTT

        2170                2190                2210
ATACTGTACAATAAAAACATTGCCTTTGAATGTTAATTTTTTGGTACAAAAATAAATTTA

        2230                2250                2270
TATGAAAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGGCCCTATTCTATAG
```

FIG.4F

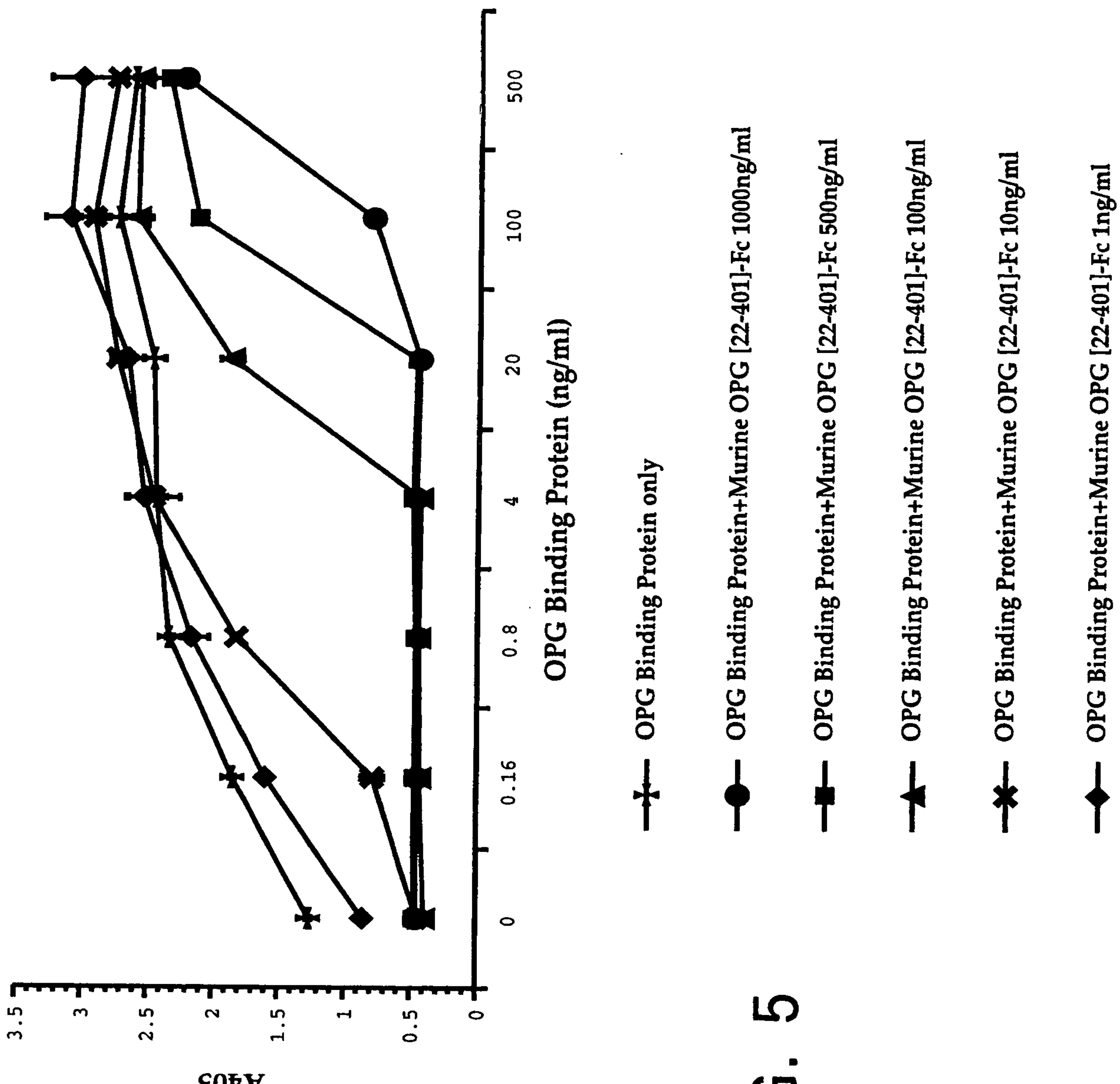

A405
3.5
3
2.5
2
1.5
1
0.5
0
0
0.16
0.8
4
20
100
500
OPG Binding Protein (ng/ml)
OPG Binding Protein only
OPG Binding Protein+Murine OPG [22-401]-Fc 1000ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 500ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 100ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 10ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 1ng/ml

FIG. 5

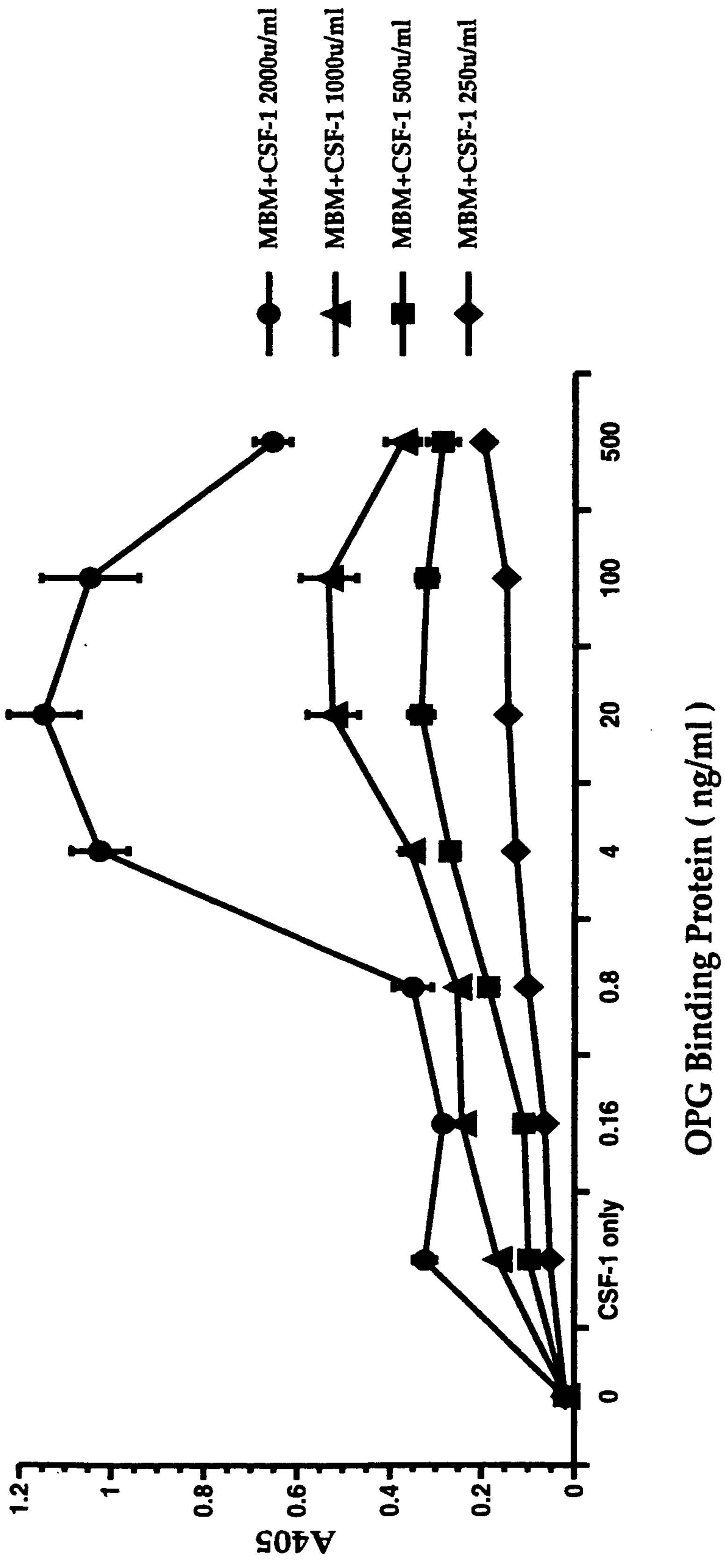

A405
1.2
1
0.8
0.6
0.4
0.2
0
0
CSF-1 only
0.16
0.8
4
20
100
500
OPG Binding Protein (ng/ml)
MBM+CSF-1 2000u/ml
MBM+CSF-1 1000u/ml
MBM+CSF-1 500u/ml
MBM+CSF-1 250u/ml

FIG. 6

FIG.7A

Toluidine Blue Staining | TRAP staining

Bone Marrow Cells + M-CSF-1

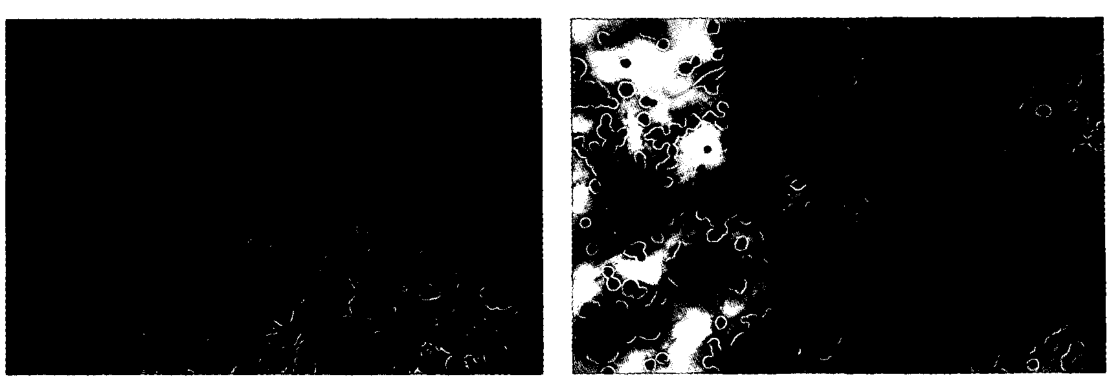
FIG.7B

Toluidine Blue Staining | TRAP staining

Bone Marrow Cells + OPG Binding Protein

FIG.7C

Toluidine Blue Staining | TRAP staining



Bone Marrow Cells + M-CSF-1 +OPG Binding Protein

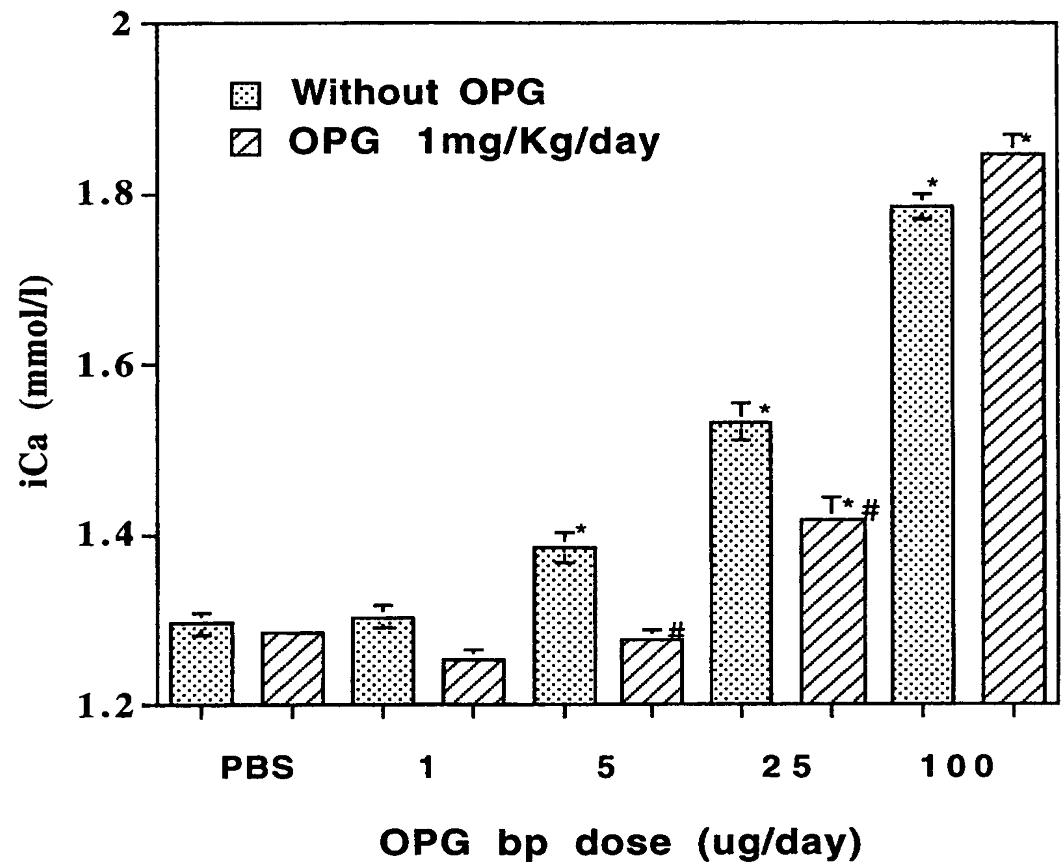

Without OPG
OPG 1mg/Kg/day
iCa (mmol/l)
2
1.8
1.6
1.4
1.2
PBS
1
5
25
100
OPG bp dose (ug/day)

FIG. 8

PBS

FIG.9A

OPGbp 5ug/d

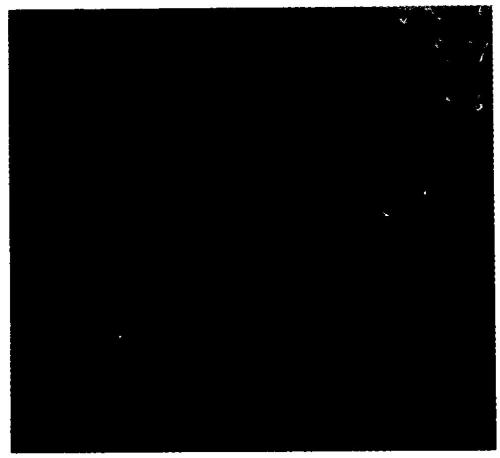


FIG.9B

OPGbp 25ug/d

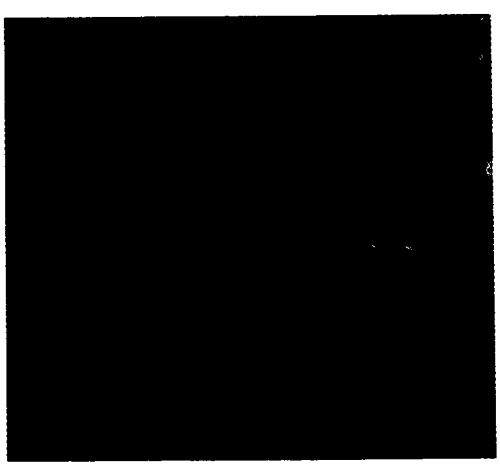


FIG.9C

OPGbp100ug/d

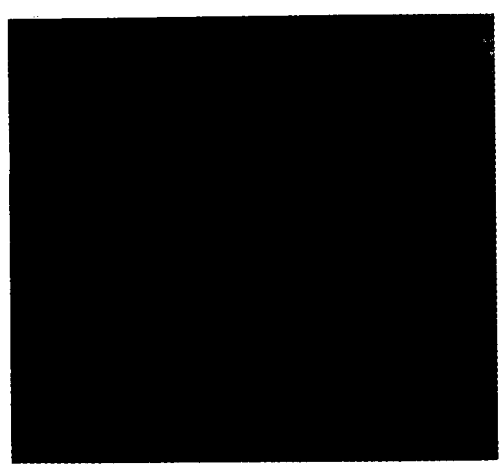


FIG.9D

```
          10                                30                                50
ACTCGACCCACGCGTCCGCCCGCCCGCACCGCGCCATGGACCCGCGCGCCCGGCGGCGCC
                                                                    M   D   P   R   A   R   R   R   R
          70                                90                                110
GCCAGCTGCCCGCGCCGCTGCTGGCGCTCTGCGTGCTGCTCGTTCCACTGCAGGTGACTC
   Q   L   P   A   P   L   L   A   L   C   V   L   L   V   P   L   Q   V   T   L
         130                               150                               170
TCCAGGTCACTCCTCCATGCACCCAGGAGAGGCATTATGAGCATCTCGGACGGTGTTGCA
   Q   V   T   P   P   C   T   Q   E   R   H   Y   E   H   L   G   R   C   C   S
         190                               210                               230
GCAGATGCGAACCAGGAAAGTACCTGTCCTCTAAGTGCACTCCTACCTCCGACAGTGTGT
   R   C   E   P   G   K   Y   L   S   S   K   C   T   P   T   S   D   S   V   C
         250                               270                               290
GTCTGCCCTGTGGCCCCGATGAGTACTTGGACACCTGGAATGAAGAAGATAAATGCTTGC
   L   P   C   G   P   D   E   Y   L   D   T   W   N   E   E   D   K   C   L   L
         310                               330                               350
TGCATAAAGTCTGTGATGCAGGCAAGGCCCTGGTGGCGGTGGATCCTGGCAACCACACGG
   H   K   V   C   D   A   G   K   A   L   V   A   V   D   P   G   N   H   T   A
```

FIG.10A

```
    370                           390                           410
CCCCGCGTCGCTGTGCTTGCACGGCTGGCTACCACTGGAACTCAGACTGCGAGTGCTGCC
 P  R  R  C  A  C  T  A  G  Y  H  W  N  S  D  C  E  C  C  R
    430                           450                           470
GCAGGAACACGGAGTGTGCACCTGGCTTCGGAGCTCAGCATCCCTTGCAGCTCAACAAGG
 R  N  T  E  C  A  P  G  F  G  A  Q  H  P  L  Q  L  N  K  D
    490                           510                           530
ATACGGTGTGCACACCCTGCCTCCTGGGCTTCTTCTCAGATGTCTTTTCGTCCACAGACA
 T  V  C  T  P  C  L  L  G  F  F  S  D  V  F  S  S  T  D  K
    550                           570                           590
AATGCAAACCTTGGACCAACTGCACCCTCCTTGGAAAGCTAGAAGCACACCAGGGGACAA
 C  K  P  W  T  N  C  T  L  L  G  K  L  E  A  H  Q  G  T  T
    610                           630                           650
CGGAATCAGATGTGGTCTGCAGCTCTTCCATGACACTGAGGAGACCACCCAAGGAGGCCC
 E  S  D  V  V  C  S  S  S  M  T  L  R  R  P  P  K  E  A  Q
```

FIG.10B

670 690 710
AGGCTTACCTGCCCAGTCTCATCGTTCTGCTCCTCTTCATCTCTGTGGTAGTAGTGGCTG
A Y L P **S L I V L L L F I S V V V V A A**

730 750 770
CCATCATCTTCGGCGTTTACTACAGGAAGGGAGGGAAAGCGCTGACAGCTAATTTGTGGA
I I F G V Y Y R K G G K A L T A N L W N

790 810 830
ATTGGGTCAATGATGCTTGCAGTAGTCTAAGTGGAAATAAGGAGTCCTCAGGGGACCGTT
W V N D A C S S L S G N K E S S G D R C

850 870 890
GTGCTGGTTCCCACTCGGCAACCTCCAGTCAGCAAGAAGTGTGTGAAGGTATCTTACTAA
A G S H S A T S S Q Q E V C E G I L L M

910 930 950
TGACTCGGGAGGAGAAGATGGTTCCAGAAGACGGTGCTGGAGTCTGTGGGCCTGTGTGTG
T R E E K M V P E D G A G V C G P V C A

970 990 1010
CGGCAGGTGGGCCCTGGGCAGAAGTCAGAGATTCTAGGACGTTCACACTGGTCAGCGAGG
A G G P W A E V R D S R T F T L V S E V

FIG.10C

```
     1030                          1050                         1070
TTGAGACGCAAGGAGACCTCTCGAGGAAGATTCCCACAGAGGATGAGTACACGGACCGGC
  E   T   Q   G   D   L   S   R   K   I   P   T   E   D   E   Y   T   D   R   P
     1090                          1110                         1130
CCTCGCAGCCTTCGACTGGTTCACTGCTCCTAATCCAGCAGGGAAGCAAATCTATACCCC
  S   Q   P   S   T   G   S   L   L   L   I   Q   Q   G   S   K   S   I   P   P
     1150                          1170                         1190
CATTCCAGGAGCCCCTGGAAGTGGGGGAGAACGACAGTTTAAGCCAGTGTTTCACCGGGA
  F   Q   E   P   L   E   V   G   E   N   D   S   L   S   Q   C   F   T   G   T
     1210                          1230                         1250
CTGAAAGCACGGTGGATTCTGAGGGCTGTGACTTCACTGAGCCTCCGAGCAGAACTGACT
  E   S   T   V   D   S   E   G   C   D   F   T   E   P   P   S   R   T   D   S
     1270                          1290                         1310
CTATGCCCGTGTCCCCTGAAAAGCACCTGACAAAAGAAATAGAAGGTGACAGTTGCCTCC
  M   P   V   S   P   E   K   H   L   T   K   E   I   E   G   D   S   C   L   P
     1330                          1350                         1370
CCTGGGTGGTCAGCTCCAACTCAACAGATGGCTACACAGGCAGTGGGAACACTCCTGGGG
  W   V   V   S   S   N   S   T   D   G   Y   T   G   S   G   N   T   P   G   E
```

FIG.10D

```
1390                1410                1430
AGGACCATGAACCCTTTCCAGGGTCCCTGAAATGTGGACCATTGCCCCAGTGTGCCTACA
 D  H  E  P  F  P  G  S  L  K  C  G  P  L  P  Q  C  A  Y  S
1450                1470                1490
GCATGGGCTTTCCCAGTGAAGCAGCAGCCAGCATGGCAGAGGCGGGAGTACGGCCCCAGG
 M  G  F  P  S  E  A  A  A  S  M  A  E  A  G  V  R  P  Q  D
1510                1530                1550
ACAGGGCTGATGAGAGGGGAGCCTCAGGGTCCGGGAGCTCCCCCAGTGACCAGCCACCTG
 R  A  D  E  R  G  A  S  G  S  G  S  S  P  S  D  Q  P  P  A
1570                1590                1610
CCTCTGGGAACGTGACTGGAAACAGTAACTCCACGTTCATCTCTAGCGGGCAGGTGATGA
 S  G  N  V  T  G  N  S  N  S  T  F  I  S  S  G  Q  V  M  N
1630                1650                1670
ACTTCAAGGGTGACATCATCGTGGTGTATGTCAGCCAGACCTCGCAGGAGGGCCCGGGTT
 F  K  G  D  I  I  V  V  Y  V  S  Q  T  S  Q  E  G  P  G  S
1690                1710                1730
CCGCAGAGCCCGAGTCGGAGCCCGTGGGCCGCCCTGTGCAGGAGGAGACGCTGGCACACA
 A  E  P  E  S  E  P  V  G  R  P  V  Q  E  E  T  L  A  H  R
```

FIG.10E

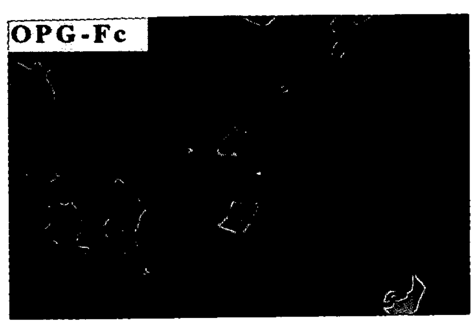
```
        1750                     1770                     1790
GAGACTCCTTTGCGGGCACCGCGCCGCTTCCCCGACGTCTGTGCCACCGGGGCTGGGC
  D  S  F  A  G  T  A  P  R  F  P  D  V  C  A  T  G  A  G  L
        1810                     1830                     1850
TGCAGGAGCAGGGGGCACCCCGGCAGAAGGACGGGACATCGCGGCCGGTGCAGGAGCAGG
  Q  E  Q  G  A  P  R  Q  K  D  G  T  S  R  P  V  Q  E  Q  G
        1870                     1890                     1910
GTGGGGCGCAGACTTCACTCCATACCCAGGGGTCCGGACAATGTGCAGAATGACCTCACC
  G  A  Q  T  S  L  H  T  Q  G  S  G  Q  C  A  E
        1930                     1950                     1970
TTCTCTGTCTGCCCTGGGTGCAGGGCACCAGTGCCTTTCCAAAAACATGGTGTAGCTAGC
        1990                     2010                     2030
CACTGTGCACCTCCTCACTGGTGCAGGCTGCTGGCATGGTGATGGAGCCCACCTCTCACT
        2050                     2070
TCCTCCAGTGCCCCTCTCCTCTGCCTCCTAC
```

FIG.10F

FIG.11A

FIG.11B

FIG.11C



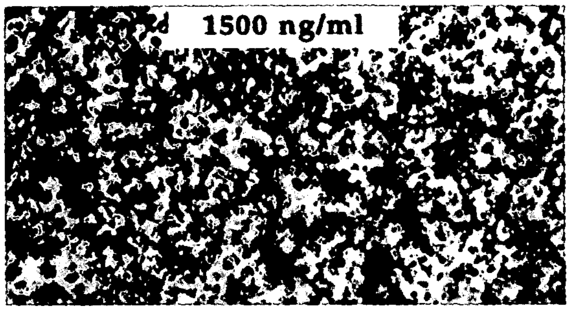


FIG.12A

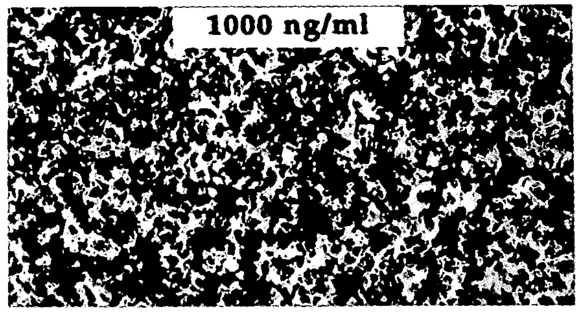


FIG.12B

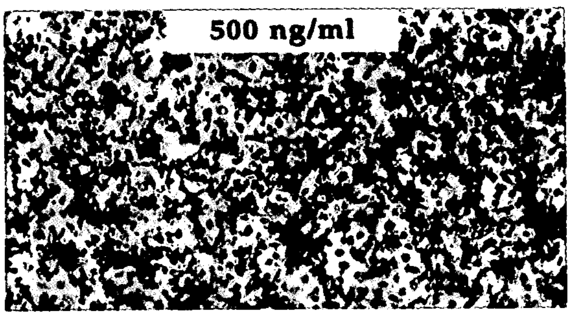


FIG.12C

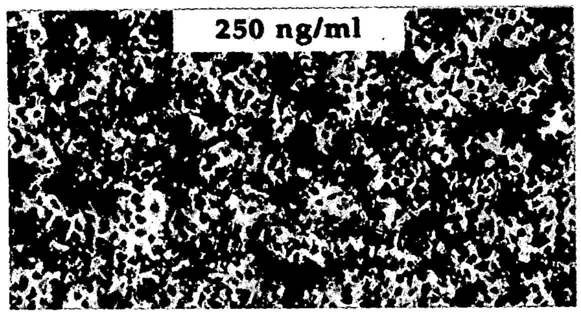


FIG.12D

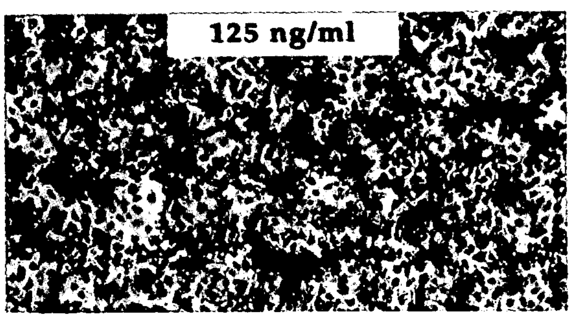


FIG.12E

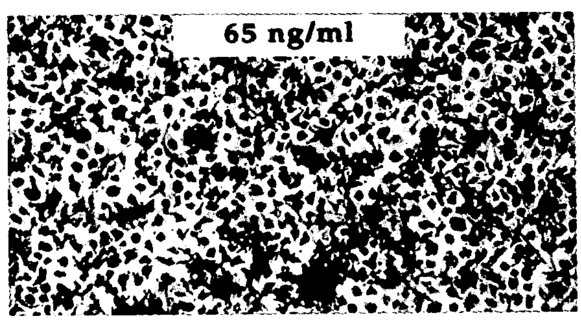


FIG.12F

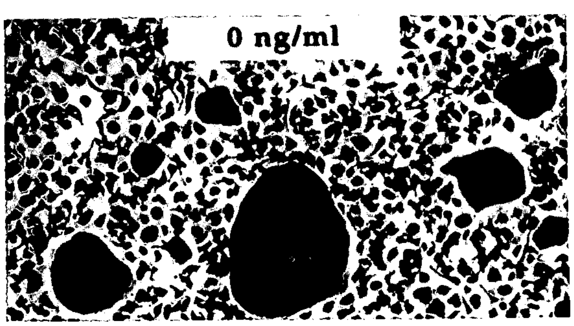
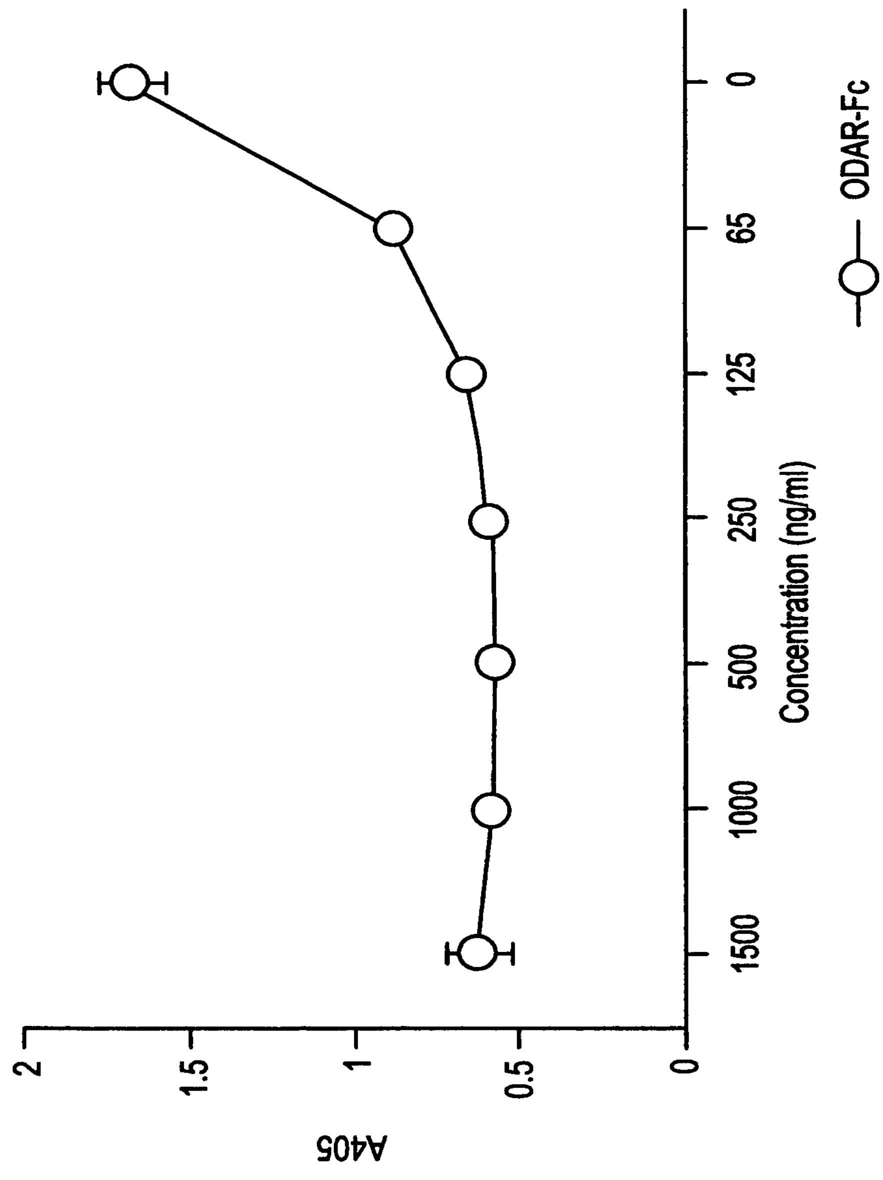
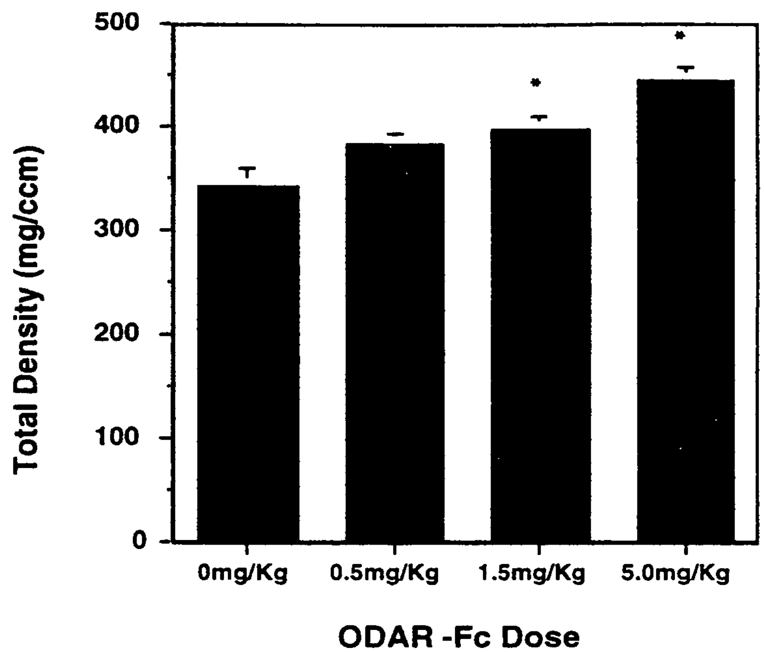


FIG.12G

FIG. 12H


A405
2
1.5
1
0.5
0
0
65
125
250
500
1000
1500
Concentration (ng/ml)
ODAR-Fc



* Different to vehicle treated control $p < 0.05$.

FIG.13